SEQUENCE LISTING

<110> Dale, James Langham
      Harding, Robert Maxwell
      Becker, Douglas Keith
      Hafner, Gregory John
      Yang, Ilin

<120> Transcriptional Control Element, Chimeric Constructs and Uses

      Therefor

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<141> 2005-01-18

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atacagatct cttagaagaa tttcaattaa cttttgcttca aattaatctt cttgaagcat     6720

ctcttcatga acgattaatg aaatgccaaa gttatgcaac gagagataat ttctggggag      6780

attggctgcc tgaagctcgc agagatcttt tgcaaattca actagccaaa gaaatcatcg      6840

agaaggttcg tgaaaagctt cactctatct agataggatt ctttgtgtgt gagtggcgca      6900

cttgcgcata atgtagtaag gaattattgt acttttacgc tggacgccac taggctccat      6960

gctttctgta atgtcacatc acttttacga attgagcctc ggggagccgt cgtacaaag       7020

tagatgcttt tctagtcaca tctgactttt ctaaaagcag atgccatcaa ctttattcga      7080

gttgagcctc ggggagccgc tcgtttaaag atgctctttt gaaaatgaca gcgcgtggtg      7140

cgatgtcatt ctcacctttt ctttaatgcg tcggccaccg actgcattat tgagattctc      7200

ttatcccttt gccacctcat cggttgcatt attgggattt cgtatcgagt cgagggacga      7260

ggcctccact actcctataa aaggacctca acccctcaga agaacggcaa gccggaaaca      7320

ccgaacttcc cattcttctc ttgagtcttt cctttgagct tgagcttgtg tgtaatcttt      7380

catagtttct aagtctccga agaacgagca ccgtctcgtg aaggagccga tccttttcca      7440

accacacttt ttctacct                                                    7458


<210>   3
<211>   146
<212>   PRT
<213>   Taro bacilliform virus
```

9

<400> 3

Met Ala Lys Lys Phe Glu Ala Ala Ile Lys Asp Trp Tyr Asp Asn Ser
1   5   10   15

Arg Arg Ala Asp Leu Ser Tyr Leu Asp Leu Ala Thr Thr Thr Lys Pro
            20   25   30

Ser Ala Ser Gln Leu Ala His Asn Leu Gln Val Ile Phe Asp Arg Leu
        35   40   45

Ser Leu His Ser Ser Val Ser Ile Lys Glu His Tyr Glu Val Val Ser
    50   55   60

Lys Leu His Ser Leu Glu Lys Ser Ile Glu Glu Leu Lys Ser Glu Leu
65   70   75   80

Thr Thr Val Lys Arg Ala Leu Thr Ser Ile Gln Lys Glu Val Phe Thr
                85   90   95

His Lys Pro Leu Thr Ala Gln Glu Val Gln Thr Leu Ala Gln Ser Leu
            100   105   110

Ile Lys Glu Pro Lys Gln Ile Glu Gln Gln Ala Val Phe Leu Leu Lys
        115   120   125

Glu Leu Lys Glu Gln Thr Ala Lys Ile Gln Ala Leu Leu His Glu Leu
    130   135   140

Lys Ser
145

<210> 4
<211> 144
<212> PRT
<213> Taro bacilliform virus

<400> 4

Met Ser Val Pro Asn Ser Thr Tyr Pro Gly Tyr Ile Lys Ser Leu Glu
1   5   10   15

Glu Thr Lys Val Leu Gly Asp Pro Ser Val Gly Phe Ser Glu Ile Pro
            20   25   30

10

```
Thr Thr Ala Ile Gly Thr Ala Thr Gly Phe Ser Thr Leu Tyr Lys Gln
        35              40                  45

Asn Asn Thr Ile Ile Asn Leu Leu Ile Ser Leu His Lys Lys Val Asp
        50              55                  60

Ser Leu Ser Lys Lys Thr Asp Val Asp Glu Leu Ala Thr Glu Leu Ser
65                  70              75                      80

Lys Leu Thr Ile Lys Asp Thr Pro Lys Val Lys Ala Lys Thr Pro Leu
                85              90                  95

Tyr Val Phe Lys Ser Pro Arg Leu Ile Leu Glu Glu Glu Arg Tyr Lys
            100             105                 110

Ile Gly Leu Pro Pro Thr Thr Thr Asp Trp Thr Trp Pro Val Gly His
        115             120                 125

Pro Phe Ala Pro Pro Pro Lys Thr Ser Thr Lys Ala Ser Thr Ser Ser
    130             135                 140


<210>  5
<211>  1881
<212>  PRT
<213>  Taro bacilliform virus

<400>  5

Met Ser Leu Ala Val Arg Asp Arg Gly Ser Asn Pro Ser Thr Ser Ser
1               5                   10                  15

Thr Val Pro Ser Gln Gln Asp Gln Ile Arg Asp Tyr Arg Asn Met Gln
            20                  25                  30

Arg Val Arg His Thr Ala Glu Arg Ala Ala Arg Arg Ile Phe Pro Gly
        35              40                  45

Arg Phe Asn Arg Thr Leu Glu Ser Gln Ile Asn Pro Glu Ala Glu Ile
    50              55                  60

Arg Leu Ser Gln Gln Arg Arg Ala Ala Met Val Pro Ala Glu Val Leu
65                  70              75                      80

Tyr Asn Thr Ser Pro Ser Thr Arg Asn Gln Lys Val Tyr Gln His Tyr
```

11

Ser Glu Glu Arg Ile Leu Cys Thr Gly Gln Asn Gln Gln Leu Asn Leu
            100   105   110

Pro Phe Ile Asn Glu Ser Ser Tyr Arg Ala Leu Arg Glu Ser Gly Gln
            115   120   125

Gln His Leu His Ile Gly Leu Ile Met Ile Arg Val His Pro Leu His
            130   135   140

Arg Arg Asn Ala Gly Thr Thr Ala Leu Ile Val Pro Arg Asp Ile Arg
145   150   155   160

Trp Asn Asp Asp Arg Ser Ile Ile Gly Thr Met Glu Ile Asp Leu Ser
                165   170   175

Ala Gly Ser Gln Ile Val Tyr Ile Ala Pro Asn Ile Met Leu Ser Val
            180   185   190

Glu Asp Phe Tyr Arg Asn Ile Gln Leu Ala Ile Gln Thr Gln Gly Tyr
            195   200   205

Glu Asn Trp Asn Ser Ala Glu Ser Asn Leu Leu Ile Ser Arg Ala Leu
            210   215   220

Ile Gly Arg Leu Thr Asn Asp Ser Phe Thr Gly Phe Gln Tyr Asn Ile
225   230   235   240

Ser Asn Val Ala Glu Tyr Leu His Ser His Gly Val Gln Ala Ile Glu
                245   250   255

Gly Gln Ala His Pro Arg Thr Leu Gly Asn Arg Trp Ile Leu Gln Ala
                260   265   270

Pro Ala Pro Pro Arg Ser Leu Val Pro Gln Asn Val Glu Thr Thr Thr
            275   280   285

Leu Leu Asp Gly Asn Val Ser Ile Arg Phe Ser Asn Tyr His Gln Ala
            290   295   300

Pro Val Asn Asp Thr Gln Asp Asn Ser His Pro Asp Ile Gln Glu Asp
305   310   315   320

12

```
Glu Asn Gln Phe Ile Gly Phe Leu Ser Asp Leu Gly Glu Glu Tyr Glu
            325             330             335

Leu Glu Tyr Pro Ser Phe Thr Pro Val His Ala Asp Glu Phe Ile Phe
            340             345             350

Ile Ile Ile Asn Gly Glu Glu Ile Pro Asp Asp Phe Val Ser Ser Phe
            355             360             365

Cys Ser Asn Phe Ser Pro Pro Pro Ile Pro Glu Pro Glu Pro Thr Ala
    370             375             380

Ile Glu Glu Thr Ala Phe Thr Leu Glu Glu Gln Phe Asn Asp Leu Asp
385             390             395             400

Tyr Pro Thr Leu Ile Ser Met Glu Lys Gln Leu Val Gln Ser Ser Val
            405             410             415

Thr Ser Ala Tyr Asn Pro Pro Thr Glu Pro Leu Met Gly Gln Val Val
            420             425             430

Tyr Pro Pro Ala Ser Ala Pro Arg Pro Gln Ala Glu Thr Ser Ser Thr
            435             440             445

Ser Glu Arg Phe Lys Asn Phe Arg Ala Lys Pro Tyr Ser Thr Pro Thr
    450             455             460

Ile Phe Leu Pro Pro Ala Tyr Asn Gln Gln Gly Ala Ile Leu Val Leu
465             470             475             480

Pro Asp Asp Ile Gly Leu Tyr Glu Asp Thr Ile Ser Arg Trp Glu Ser
            485             490             495

Ile Thr Leu Asn Met Met Asn Glu Lys Val Trp Pro Ser Asn Glu Ala
            500             505             510

Lys Ala Lys Tyr Met Glu Asn Leu Leu Gly Glu Met Glu Lys Lys Thr
            515             520             525

Trp Ile Gln Trp Arg Thr Thr Tyr Val Ser Glu Tyr Asp Ala Leu Val
    530             535             540
```

13

Gln Gln Ser Asp Glu Thr Gln Asn Leu Leu Ser Gln Val Arg Arg Ile
545   550   555   560

Phe Leu Leu Gln Asp Pro Tyr Gln Gly Ser Thr Ala Glu Gln Asp Gln
            565   570   575

Ala Tyr Asn Asp Leu Glu Arg Ile Ser Cys Asp Asn Ile Lys Asp Leu
        580   585   590

Ile Pro Tyr Leu Ile Gln Phe Arg Asn Leu Ala Ala Lys Ser Gly Arg
        595   600   605

Leu Phe Leu Gly Pro Glu Leu Ser Glu Lys Leu Phe Arg Lys Met Pro
    610   615   620

Pro Leu Ile Gly Lys Glu Ile Glu Thr Ala Phe Ile Ala Lys His Gly
625   630   635   640

Asn Ala Asn Ile Thr Val Met Pro Arg Ile His Phe Ala Tyr His Tyr
            645   650   655

Leu Ala Glu Leu Cys Lys Lys Ala Ala Leu Gln Arg Ser Leu Lys Asp
            660   665   670

Leu Ser Phe Cys Asn Gln Ile Pro Leu Pro Gly Ile Tyr Thr Lys Gly
        675   680   685

Asn Lys Lys Phe Gly Leu Arg Lys Ala Arg Thr Tyr Lys Gly Lys Pro
    690   695   700

His Pro Thr His Val Arg Val Phe Lys Lys Ala Lys Tyr Gln Arg Thr
705   710   715   720

Lys Lys Cys Lys Cys Phe Ile Cys Gly Glu Pro Gly His Phe Ala Arg
            725   730   735

Glu Cys Thr Lys Gln Arg Gly Asn Ile Val Arg Ala Thr Val His Gln
            740   745   750

Glu Leu Ala Ile Pro Asp Asn Phe Asp Val Val Ser Val Asp Ala Asp
    755   760   765

14

Glu Ser Asp Ser Ser Gly Ile Tyr Ser Tyr Ser Glu Asn Glu Ala Pro
    770   775   780

Leu Gln Glu Val Asn Ser Phe Ile His Asp Glu Asn Ile Phe Phe Leu
785   790   795   800

Ser Asp Ala Asp Glu Phe Glu Ser Pro Gln Gln His Leu His Glu Thr
            805   810   815

Val Asn Met Leu Gln Ser Arg Ser Ala Tyr Leu Pro Gln Val Ala Val
        820   825   830

Gly Glu Glu Lys Leu Asn Cys Ser His Ile Trp Leu Gln Asp Val Asp
    835   840   845

Ile Pro Ser Asp Lys His Lys Cys His Thr Cys Arg Arg Asp Thr Gln
    850   855   860

Lys His Tyr Arg Leu Glu Cys Gln Lys Cys Lys Phe Leu Val Cys Ser
865   870   875   880

Leu Cys Thr Ile Pro Tyr Leu Gly Ile Thr Met Gln Phe Arg Gln Lys
            885   890   895

Gln Lys Ser Gln Pro Glu Asn Pro Asn Leu Val Arg Glu Leu Leu Glu
            900   905   910

His Ala Ile Phe Leu Glu Glu Lys Cys Lys Asn Gln Glu Leu Leu Ser
        915   920   925

Glu Thr Gln Ile Glu Arg Ile Val Ser Ser Glu Lys Gln Val Lys Phe
    930   935   940

Tyr Gly Ile Leu Pro Thr Lys Lys Ser Asn Lys Ser Ala Gly Tyr Asp
945   950   955   960

Leu Gln Ser Asn Ile Asp Ile Glu Ile Pro Pro Gly Lys Cys Thr Val
            965   970   975

Ile Ser Thr Gly Thr Phe Leu Gln Met Pro Asp Asn Met Tyr Gly Arg
            980   985   990

Leu Val Glu Arg Thr Ser Leu Ala Ile Gln Gly Ile Thr Val Gln Gly

15

Gly Val Ile Asp Pro Asp Phe Thr Gly Glu Ile Gln Ile Val Leu
       1010   1015   1020

Phe Asn His Asn Thr Ala Pro Tyr Pro Val Lys Lys Thr Tyr Arg
       1025   1030   1035

Leu Ala Gln Ile Ile Phe Glu Lys Phe Tyr Thr Pro Ile Phe Ile
       1040   1045   1050

Gln Glu Pro Phe Thr Ser Thr Gln Gln Gly Ser Ser Asn Phe Gly
       1055   1060   1065

Ser Thr Ala Lys Pro Leu Gln Ile Thr Glu Asn Ile Glu Val Met
       1070   1075   1080

Ser Glu Thr Val Ala Asn Gln Val Ala Lys Ser Ser Val Leu Pro
       1085   1090   1095

Arg Leu Tyr Ser Ile Gln Ala His Ile His Ile Ala Pro Asp Ile
       1100   1105   1110

Val Ile Ser Thr Thr Ala Ile Ile Asp Thr Gly Ala Thr Val Cys
       1115   1120   1125

Cys Ile Ser Glu Lys Ile Val Pro Glu Ala Ala Lys Glu Gln Leu
       1130   1135   1140

Asn Tyr Lys Val Asn Ile Ser Gly Ile Ser Ser Gln Gln Gln Ile
       1145   1150   1155

Gln His Arg Leu Lys Arg Gly Thr Leu Glu Ile Ala Ser Asn Lys
       1160   1165   1170

Tyr Ala Leu Pro Leu Cys Tyr Ile Ile Glu Leu Asn Asp Lys Asp
       1175   1180   1185

Asp Phe Ser Met Ile Leu Gly Cys Asn Phe Phe Lys His Met Gly
       1190   1195   1200

Gly Gly Met Arg Phe Glu Gly Pro His Val Thr Phe Tyr Lys Gly
       1205   1210   1215

```
Ile Thr  Thr Leu Ser Thr Ser  Tyr Ala Asn Thr Gly  Ile Asp Thr
    1220             1225             1230


Glu His  Glu Gln Ile Thr Ser  Thr Thr Ser Gln Ser  Phe Lys Glu
    1235             1240             1245


Arg Phe  Ser Pro Leu Met Asn  Glu Leu Lys Ala Ala  Gly Tyr Ile
    1250             1255             1260


Gly Glu  Asp Pro Leu Lys His  Trp Ser Lys Asn Lys  Val Thr Cys
    1265             1270             1275


Lys Leu  Asp Leu Lys Asn Thr  Glu Ile Thr Ile Gln  Asp Lys Pro
    1280             1285             1290


Leu Arg  His Ile Thr Pro Ala  Leu Glu Gln Ser Tyr  Gly Arg His
    1295             1300             1305


Val Asn  Ala Leu Leu Met Leu  Lys Val Ile Gln Pro  Ser Lys Ser
    1310             1315             1320


Arg His  Arg Thr Met Ala Phe  Leu Val Asn Ser Gly  Thr Thr Val
    1325             1330             1335


Thr Ala  Asp Gly Lys Glu Ile  Lys Gly Lys Glu Arg  Met Val Phe
    1340             1345             1350


Asn Tyr  Lys Ala Leu Asn Asp  Asn Thr Tyr Lys Asp  Gln Tyr Ser
    1355             1360             1365


Leu Pro  Asn Ile Gln Leu Ile  Leu Lys Lys Val Ile  Asn Ser Thr
    1370             1375             1380


Ile Tyr  Ser Lys Phe Asp Leu  Lys Ser Gly Phe His  Gln Val Ala
    1385             1390             1395


Met Asp  Pro Asp Ser Val Glu  Trp Thr Ala Phe Leu  Val Pro Gln
    1400             1405             1410


Gly Leu  Tyr Glu Trp Leu Ala  Met Pro Phe Gly Leu  Lys Asn Ala
    1415             1420             1425
```

17

Pro Ala Val Phe Gln Arg Lys Met Asp Ala Val Phe Lys Gly Cys
    1430   1435   1440

Glu Lys Phe Leu Ala Val Tyr Ile Asp Asp Ile Leu Val Phe Ser
    1445   1450   1455

Asn Asn Glu Glu Asp His Ala Lys His Leu Val Ile Met Leu Gln
    1460   1465   1470

Arg Cys Lys Glu His Gly Leu Val Leu Ser Pro Thr Lys Met Asn
    1475   1480   1485

Ile Ala Val Arg Glu Val Asn Phe Leu Gly Ala Thr Ile Gly Ser
    1490   1495   1500

Arg Lys Val Lys Leu Gln Glu Asn Ile Ile Lys Lys Ile Leu Asp
    1505   1510   1515

Phe Asp Thr Glu Lys Leu Gln Ser Lys Lys Gly Leu Arg Ser Phe
    1520   1525   1530

Leu Gly Ile Leu Asn Tyr Ala Arg Asn His Ile Pro Asn Leu Gly
    1535   1540   1545

Lys Ile Ala Gly Pro Leu Tyr Ser Lys Thr Ser Ile Tyr Gly Asp
    1550   1555   1560

Ile Arg Phe Ser Ala Ser Asp Trp Lys Leu Ile Asn Glu Ile Lys
    1565   1570   1575

Ala Ile Val Glu Lys Leu Pro Pro Leu Asp Tyr Pro Pro Glu Gln
    1580   1585   1590

Ala Tyr Ile Ile Ile Glu Ser Asp Gly Cys Met Glu Gly Trp Gly
    1595   1600   1605

Ala Ile Cys Lys Trp Lys Leu Ala Glu Tyr Asp Pro Lys Ser Ser
    1610   1615   1620

Glu Gln Ile Cys Ala Tyr Ala Ser Gly Lys Phe Ser Pro Ile Lys
    1625   1630   1635

18

Ser Thr Ile Asp Ala Glu Ile Thr Ala Ala Met Glu Gly Leu Glu
    1640   1645   1650

Ala Phe Lys Ile His Tyr Leu Asp Lys Gln Lys Ile Thr Leu Arg
    1655   1660   1665

Thr Asp Cys Gln Ala Ile Ile Ser Phe Cys Asn Lys Thr Ser Val
    1670   1675   1680

Asn Lys Pro Ser Arg Val Arg Trp Leu Lys Phe Ile Asp Tyr Ile
    1685   1690   1695

Thr Asn Thr Gly Ile Asp Val Lys Phe Glu His Ile Asp Ala Lys
    1700   1705   1710

Asn Asn Val Leu Ala Asp Thr Leu Ser Arg Leu Val Asn Thr Leu
    1715   1720   1725

Gln Asp Leu Pro Trp Leu Asp Glu Pro His Gln Asp Gln Thr Val
    1730   1735   1740

Ser Leu Met Gln Glu Ile Glu Asp Ala Pro Leu Glu Ile Lys Gln
    1745   1750   1755

Arg Ser Leu Thr Cys Leu Gln Arg Leu Ile Cys Arg Ser Phe Met
    1760   1765   1770

Glu Asp Ser Thr Glu Glu Ala Ile His Phe Leu Glu Asp Asp Lys
    1775   1780   1785

Ile Glu Pro Thr Ala Glu Ser Ser Thr Pro Ile Thr Leu Asp Glu
    1790   1795   1800

Phe Ser Arg Lys Arg Phe Gln Glu His Thr Asp Leu Leu Glu Glu
    1805   1810   1815

Phe Gln Leu Thr Leu Leu Gln Ile Asn Leu Leu Glu Ala Ser Leu
    1820   1825   1830

His Glu Arg Leu Met Lys Cys Gln Ser Tyr Ala Thr Arg Asp Asn
    1835   1840   1845

Phe Trp Gly Asp Trp Leu Pro Glu Ala Arg Arg Asp Leu Leu Gln

19

```
          1850                    1855                           1860


Ile Gln  Leu Ala Lys Glu Ile  Ile Glu Lys Val Arg  Glu Lys Leu
     1865                    1870                    1875


His Ser  Ile
     1880


<210>  6
<211>  1190
<212>  DNA
<213>  Taro bacilliform virus

<400>  6
gccttcacgg gttagatggt tgaagttcat tgattatatt actaacactg gaattgatgt      60

taaatttgaa catattgatg ctaaaaataa tgtcttagct gacactctgt ccaggttagt     120

taacactttg caggatttgc catggctaga tgaacctcat caggatcaaa cagtctccct     180

gatgcaggaa attgaagatg cacctcttga aatcaagcag cgttctttaa cctgcttaca     240

gagactgatc tgtagaagct tcatggaaga ttctacagaa gaagctattc acttcctcga     300

agatgataag atcgagccaa cagctgagtc atcaacccca attactttgg atgaattttc     360

aagaaaaga ttccaagaac atacagatct cttagaagaa tttcaattaa ctttgcttca     420

aattaatctt cttgaagcat ctcttcatga acgattaatg aaatgccaaa gttatgcaac     480

gagagataat ttctggggag attggctgcc tgaagctcgc agagatcttt tgcaaattca     540

actagccaaa gaaatcatcg agaaggttcg tgaaaagctt cactctatct agataggatt     600

ctttgtgtgt gagtggcgca cttgcgcata atgtagtaag gaattattgt acttttacgc     660

tggacgccac taggctccat gctttctgta atgtcacatc acttttacga attgagcctc     720

ggggagccgt tcgtacaaag tagatgcttt tctagtcaca tctgactttt ctaaaagcag     780

atgccatcaa ctttattcga gttgagcctc ggggagccgc tcgtttaaag atgctctttt     840

gaaaatgaca gcgcgtggtg cgatgtcatt ctcacctttt ctttaatgcg tcggccaccg     900

actgcattat tgagattctc ttatcccttt gccacctcat cggttgcatt attgggattt     960

cgtatcgagt cgagggacga ggcctccact actcctataa aaggacctca acccctcaga    1020

agaacggcaa gccggaaaca ccgaacttcc cattcttctc ttgagtcttt cctttgagct    1080

tgagcttgtg tgtaatcttt catagtttct aagtctccga agaacgagca ccgtctcgtg    1140

aaggagccga tccttttcca accacacttt ttctaccttg gtatcagagc                1190
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20

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<210>    7
<211>    598
<212>    DNA
<213>    Taro bacilliform virus

<400>    7
ataggattct ttgtgtgtga gtggcgcact tgcgcataat gtagtaagga attattgtac        60

ttttacgctg gacgccacta ggctccatgc tttctgtaat gtcacatcac ttttacgaat       120

tgagcctcgg ggagccgttc gtacaaagta gatgcttttc tagtcacatc tgacttttct       180

aaaagcagat gccatcaact ttattcgagt tgagcctcgg ggagccgctc gtttaaagat       240

gctcttttga aaatgacagc gcgtggtgcg atgtcattct caccttttct ttaatgcgtc       300

ggccaccgac tgcattattg agattctctt atccctttgc cacctcatcg gttgcattat       360

tgggatttcg tatcgagtcg agggacgagg cctccactac tcctataaaa ggacctcaac       420

ccctcagaag aacggcaagc cggaaacacc gaacttccca ttcttctctt gagtctttcc       480

tttgagcttg agcttgtgtg taatctttca tagtttctaa gtctccgaag aacgagcacc       540

gtctcgtgaa ggagccgatc cttttccaac cacacttttt ctaccttggt atcagagc        598


<210>    8
<211>    529
<212>    DNA
<213>    Taro bacilliform virus

<400>    8
ggacgccact aggctccatg ctttctgtaa tgtcacatca cttttacgaa ttgagcctcg        60

gggagccgtt cgtacaaagt agatgctttt ctagtcacat ctgacttttc taaaagcaga       120

tgccatcaac tttattcgag ttgagcctcg gggagccgct cgtttaaaga tgctcttttg       180

aaaatgacag cgcgtggtgc gatgtcattc tcaccttttc tttaatgcgt cggccaccga       240

ctgcattatt gagattctct tatccctttg ccacctcatc ggttgcatta ttgggatttc       300

gtatcgagtc gagggacgag gcctccacta ctcctataaa aggacctcaa cccctcagaa       360

gaacggcaag ccggaaacac cgaacttccc attcttctct tgagtctttc ctttgagctt       420

gagcttgtgt gtaatctttc atagtttcta agtctccgaa gaacgagcac cgtctcgtga       480

aggagccgat ccttttccaa ccacactttt tctaccttgg tatcagagc                   529


<210>    9
<211>    261
<212>    DNA
<213>    Taro bacilliform virus
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21

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<400>  9
tgccacctca tcggttgcat tattgggatt tcgtatcgag tcgagggacg aggcctccac      60

tactcctata aaaggacctc aaccccctcag aagaacggca agccggaaac accgaacttc     120

ccattcttct cttgagtctt tcctttgagc ttgagcttgt gtgtaatctt tcatagtttc     180

taagtctccg aagaacgagc accgtctcgt gaaggagccg atccttttcc aaccacactt     240

tttctacctt ggtatcagag c                                               261


<210>  10
<211>  20
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Badna FP primer


<220>
<221>  modified_base
<222>  (5)..(6)
<223>  I

<220>
<221>  modified_base
<222>  (10)..(11)
<223>  I

<220>
<221>  modified_base
<222>  (18)..(19)
<223>  I

<400>  10
atgccttygg aaraaygccc                                                  20


<210>  11
<211>  20
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Badna RP primer


<220>
<221>  modified_base
<222>  (9)..(10)
<223>  I

<220>
<221>  modified_base
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<222>  (11)..(12)
<223>  I

<220>
<221>  modified_base
<222>  (13)..(14)
<223>  I

<220>
<221>  modified_base
<222>  (18)..(19)
<223>  I

<400>  11
ccayttrcaa cscccccacc                                            20


<210>  12
<211>  23
<212>  DNA
<213>  Artificial Sequence

<220>

<223>  1F primer

<400>  12
ggatgcagta ttcaaagggt gtg                                        23


<210>  13
<211>  26
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  TRBR primer

<400>  13
ctgcaggcgg ccgcgctctg atacca                                     26


<210>  14
<211>  22
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  5F primer

<400>  14
agtctttcct ttgagcttga gc                                         22


<210>  15
<211>  25
<212>  DNA
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<213> Artificial Sequence

<220>
<223> G2R primer

<400> 15
cacacccttt gaatactgca tccat   25

<210> 16
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Cytoplasmic initiator methionine tRNA (tRNAmet) binding site

<400> 16
tggtatcaga gc   12

<210> 17
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> F-GTN primer

<400> 17
ctgcagatag gattctttgt gtgtg   25

<210> 18
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> R-GTN primer

<400> 18
ccatgggctc tgataccaag gtag   24

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> P527-F primer

<400> 19
ctgcagggac gccactaggc   20

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<210>   20
<211>   23
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   P257-F primer

<400>   20
ctgcaggcca cctcatcggt tgc                                                    23


<210>   21
<211>   23
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   P114-F primer

<400>   21
ctgcaggagc ttgagcttgt gtg                                                    23


<210>   22
<211>   24
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   FP-as-1 primer

<400>   22
ctgcaggcct tcacgggtta gatg                                                   24


<210>   23
<211>   24
<212>   DNA
<213>   Artificial Sequence


<220>
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27